



IFWO

RAW SEQUENCE LISTING

DATE: 08/02/2004

PATENT APPLICATION: US/10/829,250

TIME: 14:37:42

Input Set : N:\CrF3\RULE60\10829250.raw

Output Set: N:\CRF4\08022004\J829250.raw

1 <110> APPLICANT: HATTORI, NORIAKI
 2 MURAKAMI, SEIJI
 3 <120> TITLE OF INVENTION: LUCIFERASE AND A METHOD FOR DETECTING INTRACELLULAR ATP
 USING THE
 4 SAME
 5 <130> FILE REFERENCE: 193582US-3524-7126-0 PCT
 6 <140> CURRENT APPLICATION NUMBER: US/10/829,250
 7 <141> CURRENT FILING DATE: 2004-04-22
 8 <150> PRIOR APPLICATION NUMBER: US/09/581,241
 9 <151> PRIOR FILING DATE: 2000-06-26
 10 <150> PRIOR APPLICATION NUMBER: JP97/361022
 11 <151> PRIOR FILING DATE: 1997-12-26
 12 <160> NUMBER OF SEQ ID NOS: 8
 13 <170> SOFTWARE: PatentIn version 3.2
 15 <210> SEQ ID NO: 1
 16 <211> LENGTH: 23
 17 <212> TYPE: DNA
 18 <213> ORGANISM: ARTIFICIAL SEQUENCE
 19 <220> FEATURE:
 20 <223> OTHER INFORMATION: SYNTHETIC DNA
 21 <400> SEQUENCE: 1
 22 tggtgtactt aagaaaggaa aat 23
 24 <210> SEQ ID NO: 2
 25 <211> LENGTH: 23
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 30 <400> SEQUENCE: 2
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 34 <211> LENGTH: 1644
 35 <212> TYPE: DNA
 36 <213> ORGANISM: Luciola lateralis
 37 <220> FEATURE:
 38 <221> NAME/KEY: CDS
 39 <222> LOCATION: (1)..(1644)
 40 <400> SEQUENCE: 3
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 42 Met Glu Asn Met Glu Asn Asp Glu Asn Ile Val Tyr Gly Pro Glu Pro
 43 1 5 10 15
 44 ttt tac cct att gaa gag gga tct gct gga gca caa ttg cgc aag tat 96
 45 Phe Tyr Pro Ile Glu Glu Gly Ser Ala Gly Ala Gln Leu Arg Lys Tyr
 46 20 25 30

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47	atg gat cga tat gca aaa ctt gga gca att gct ttt act aac gca ctt	144
48	Met Asp Arg Tyr Ala Lys Leu Gly Ala Ile Ala Phe Thr Asn Ala Leu	
49	35 40 45	
50	acc ggt gtc gat tat acg tac gcc gaa tac tta gaa aaa tca tgc tgt	192
51	Thr Gly Val Asp Tyr Thr Tyr Ala Glu Tyr Leu Glu Lys Ser Cys Cys	
52	50 55 60	
53	cta gga gag gct tta aag aat tat ggt ttg gtt gtt gat gga aga att	240
54	Leu Gly Glu Ala Leu Lys Asn Tyr Gly Leu Val Val Asp Gly Arg Ile	
55	65 70 75 80	
56	gcg tta tgc agt gaa aac tgt gaa gaa ttc ttt att cct gta tta gcc	288
57	Ala Leu Cys Ser Glu Asn Cys Glu Glu Phe Phe Ile Pro Val Leu Ala	
58	85 90 95	
59	ggt tta ttt ata ggt gtc ggt gtg gct cca act aat gag att tac act	336
60	Gly Leu Phe Ile Gly Val Gly Val Ala Pro Thr Asn Glu Ile Tyr Thr	
61	100 105 110	
62	cta cgt gaa ttg gtt cac agt tta ggc atc tct aag cca aca att gta	384
63	Leu Arg Glu Leu Val His Ser Leu Gly Ile Ser Lys Pro Thr Ile Val	
64	115 120 125	
65	ttt agt tct aaa aaa gga tta gat aaa gtt ata act gta caa aaa acg	432
66	Phe Ser Ser Lys Lys Gly Leu Asp Lys Val Ile Thr Val Gln Lys Thr	
67	130 135 140	
68	gta act gct att aaa acc att gtt ata ttg gac agc aaa gtg gat tat	480
69	Val Thr Ala Ile Lys Thr Ile Val Ile Leu Asp Ser Lys Val Asp Tyr	
70	145 150 155 160	
71	aga ggt tat caa tcc atg gac aac ttt att aaa aaa aac act cca caa	528
72	Arg Gly Tyr Gln Ser Met Asp Asn Phe Ile Lys Lys Asn Thr Pro Gln	
73	165 170 175	
74	ggt ttc aaa gga tca agt ttt aaa act gta gaa gtt aac cgc aaa gaa	576
75	Gly Phe Lys Gly Ser Ser Phe Lys Thr Val Glu Val Asn Arg Lys Glu	
76	180 185 190	
77	caa gtt gct ctt ata atg aac tct tcg ggt tca acc ggt ttg cca aaa	624
78	Gln Val Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys	
79	195 200 205	
80	ggt gtg caa ctt act cat gaa aat ttg gtc act aga ttt tct cac gct	672
81	Gly Val Gln Leu Thr His Glu Asn Leu Val Thr Arg Phe Ser His Ala	
82	210 215 220	
83	aga gat cca att tat gga aac caa gtt tca cca ggc acg gct att tta	720
84	Arg Asp Pro Ile Tyr Gly Asn Gln Val Ser Pro Gly Thr Ala Ile Leu	
85	225 230 235 240	
86	act gta gta cca ttc cat cat ggt ttt ggt atg ttt act act tta ggc	768
87	Thr Val Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly	
88	245 250 255	
89	tat cta act tgt ggt ttt cgt att gtc atg tta acg aaa ttt gac gaa	816
90	Tyr Leu Thr Cys Gly Phe Arg Ile Val Met Leu Thr Lys Phe Asp Glu	
91	260 265 270	
92	gag act ttt tta aaa aca ctg caa gat tac aaa tgt tca agc gtt att	864
93	Glu Thr Phe Leu Lys Thr Leu Gln Asp Tyr Lys Cys Ser Ser Val Ile	
94	275 280 285	
95	ctt gta ccg act ttg ttt gca att ctt aat aga agt gaa tta ctc gat	912

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Input Set : N:\Crif3\RULE60\10829250.raw

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96	Leu Val Pro Thr Leu Phe Ala Ile Leu Asn Arg Ser Glu Leu Leu Asp	
97	290 295 300	
98	aaa tat gat tta tca aat tta gtt gaa att gca tct ggc gga gca cct	960
99	Lys Tyr Asp Leu Ser Asn Leu Val Glu Ile Ala Ser Gly Gly Ala Pro	
100	305 310 315 320	
101	tta tct aaa gaa att ggt gaa gct gtt gct aga cgt ttt aat tta ccg	1008
102	Leu Ser Lys Glu Ile Gly Glu Ala Val Ala Arg Arg Phe Asn Leu Pro	
103	325 330 335	
104	ggg gtt cgt caa ggc tat ggt tta aca gaa aca acc tct gca att att	1056
105	Gly Val Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Ile	
106	340 345 350	
107	atc aca ccg gaa ggc gat gat aaa cca ggt gct tct ggc aaa gtt gtg	1104
108	Ile Thr Pro Glu Gly Asp Asp Lys Pro Gly Ala Ser Gly Lys Val Val	
109	355 360 365	
110	cca tta ttt aaa gca aaa gtt atc gat ctt gat act aaa aaa act ttg	1152
111	Pro Leu Phe Lys Ala Lys Val Ile Asp Leu Asp Thr Lys Lys Thr Leu	
112	370 375 380	
113	ggc ccg aac aga cgt gga gaa gtt tgt gta aag ggt cct atg ctt atg	1200
114	Gly Pro Asn Arg Arg Gly Glu Val Cys Val Lys Gly Pro Met Leu Met	
115	385 390 395 400	
116	aaa ggt tat gta gat aat cca gaa gca aca aga gaa atc ata gat gaa	1248
117	Lys Gly Tyr Val Asp Asn Pro Glu Ala Thr Arg Glu Ile Ile Asp Glu	
118	405 410 415	
119	gaa ggt tgg ttg cac aca gga gat att ggg tat tac gat gaa gaa aaa	1296
120	Glu Gly Trp Leu His Thr Gly Asp Ile Gly Tyr Tyr Asp Glu Glu Lys	
121	420 425 430	
122	cat ttc ttt atc gtg gat cgt ttg aag tct tta atc aaa tac aaa gga	1344
123	His Phe Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly	
124	435 440 445	
125	tat caa gta cca cct gct gaa tta gaa tct gtt ctt ttg caa cat cca	1392
126	Tyr Gln Val Pro Pro Ala Glu Leu Glu Ser Val Leu Leu Gln His Pro	
127	450 455 460	
128	aat att ttt gat gcc ggc gtt gct ggc gtt cca gat cct ata gct ggt	1440
129	Asn Ile Phe Asp Ala Gly Val Ala Gly Val Pro Asp Pro Ile Ala Gly	
130	465 470 475 480	
131	gag ctt ccg gga gct gtt gtt gta ctt aag aaa gga aaa tct atg act	1488
132	Glu Leu Pro Gly Ala Val Val Val Leu Lys Lys Gly Lys Ser Met Thr	
133	485 490 495	
134	gaa aaa gaa gta atg gat tac gtt gct agt caa gtt tca aat gca aaa	1536
135	Glu Lys Glu Val Met Asp Tyr Val Ala Ser Gln Val Ser Asn Ala Lys	
136	500 505 510	
137	cgt ttg cgt ggt ggt gtc cgt ttt gtg gac gaa gta cct aaa ggt ctc	1584
138	Arg Leu Arg Gly Gly Val Arg Phe Val Asp Glu Val Pro Lys Gly Leu	
139	515 520 525	
140	act ggt aaa att gac ggt aaa gca att aga gaa ata ctg aag aaa cca	1632
141	Thr Gly Lys Ile Asp Gly Lys Ala Ile Arg Glu Ile Leu Lys Lys Pro	
142	530 535 540	
143	gtt gct aag atg	1644
144	Val Ala Lys Met	

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145      545
147 <210> SEQ ID NO: 4
148 <211> LENGTH: 548
149 <212> TYPE: PRT
150 <213> ORGANISM: Luciola lateralis
151 <400> SEQUENCE: 4
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154      Phe Tyr Pro Ile  Glu Glu Gly  Ser Ala Gly Ala Gln Leu Arg Lys Tyr
155              20              25              30
156      Met Asp Arg Tyr  Ala Lys Leu  Gly Ala Ile Ala Phe Thr Asn Ala Leu
157              35              40              45
158      Thr Gly Val Asp Tyr Thr Tyr Ala Glu Tyr Leu Glu Lys Ser Cys Cys
159              50              55              60
160      Leu Gly Glu Ala  Leu Lys Asn Tyr Gly Leu Val Val Asp Gly Arg Ile
161      65              70              75              80
162      Ala Leu Cys Ser  Glu Asn Cys Glu Glu Phe Phe Ile Pro Val Leu Ala
163              85              90              95
164      Gly Leu Phe Ile  Gly Val Gly Val Ala Pro Thr Asn Glu Ile Tyr Thr
165              100             105             110
166      Leu Arg Glu Leu Val His Ser Leu Gly Ile Ser Lys Pro Thr Ile Val
167              115             120             125
168      Phe Ser Ser Lys Lys Gly Leu Asp Lys Val Ile Thr Val Gln Lys Thr
169              130             135             140
170      Val Thr Ala Ile  Lys Thr Ile Val Ile Leu Asp Ser Lys Val Asp Tyr
171      145             150             155             160
172      Arg Gly Tyr Gln Ser Met Asp Asn Phe Ile Lys Lys Asn Thr Pro Gln
173              165             170             175
174      Gly Phe Lys Gly Ser Ser Phe Lys Thr Val Glu Val Asn Arg Lys Glu
175              180             185             190
176      Gln Val Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys
177              195             200             205
178      Gly Val Gln Leu Thr His Glu Asn Leu Val Thr Arg Phe Ser His Ala
179              210             215             220
180      Arg Asp Pro Ile Tyr Gly Asn Gln Val Ser Pro Gly Thr Ala Ile Leu
181      225             230             235             240
182      Thr Val Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly
183              245             250             255
184      Tyr Leu Thr Cys Gly Phe Arg Ile Val Met Leu Thr Lys Phe Asp Glu
185              260             265             270
186      Glu Thr Phe Leu Lys Thr Leu Gln Asp Tyr Lys Cys Ser Ser Val Ile
187              275             280             285
188      Leu Val Pro Thr Leu Phe Ala Ile Leu Asn Arg Ser Glu Leu Leu Asp
189              290             295             300
190      Lys Tyr Asp Leu Ser Asn Leu Val Glu Ile Ala Ser Gly Gly Ala Pro
191      305             310             315             320
192      Leu Ser Lys Glu Ile Gly Glu Ala Val Ala Arg Arg Phe Asn Leu Pro
193              325             330             335
194      Gly Val Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Ile

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195          340          345          350
196   Ile Thr Pro Glu Gly Asp Asp Lys Pro Gly Ala Ser Gly Lys Val Val
197          355          360          365
198   Pro Leu Phe Lys Ala Lys Val Ile Asp Leu Asp Thr Lys Lys Thr Leu
199          370          375          380
200   Gly Pro Asn Arg Arg Gly Glu Val Cys Val Lys Gly Pro Met Leu Met
201          385          390          395          400
202   Lys Gly Tyr Val Asp Asn Pro Glu Ala Thr Arg Glu Ile Ile Asp Glu
203          405          410          415
204   Glu Gly Trp Leu His Thr Gly Asp Ile Gly Tyr Tyr Asp Glu Glu Lys
205          420          425          430
206   His Phe Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly
207          435          440          445
208   Tyr Gln Val Pro Pro Ala Glu Leu Glu Ser Val Leu Leu Gln His Pro
209          450          455          460
210   Asn Ile Phe Asp Ala Gly Val Ala Gly Val Pro Asp Pro Ile Ala Gly
211          465          470          475          480
212   Glu Leu Pro Gly Ala Val Val Val Leu Lys Lys Gly Lys Ser Met Thr
213          485          490          495
214   Glu Lys Glu Val Met Asp Tyr Val Ala Ser Gln Val Ser Asn Ala Lys
215          500          505          510
216   Arg Leu Arg Gly Gly Val Arg Phe Val Asp Glu Val Pro Lys Gly Leu
217          515          520          525
218   Thr Gly Lys Ile Asp Gly Lys Ala Ile Arg Glu Ile Leu Lys Lys Pro
219          530          535          540
220   Val Ala Lys Met
221          545
223 <210> SEQ ID NO: 5
224 <211> LENGTH: 1644
225 <212> TYPE: DNA
226 <213> ORGANISM: Luciola lateralis
227 <220> FEATURE:
228 <221> NAME/KEY: CDS
229 <222> LOCATION: (1)..(1644)
230 <400> SEQUENCE: 5
231   atg gaa aac atg gag aac gat gaa aat att gtg tat ggt cct gaa cca      48
232   Met Glu Asn Met Glu Asn Asp Glu Asn Ile Val Tyr Gly Pro Glu Pro
233   1          5          10          15
234   ttt tac cct att gaa gag gga tct gct gga gca caa ttg cgc aag tat      96
235   Phe Tyr Pro Ile Glu Glu Gly Ser Ala Gly Ala Gln Leu Arg Lys Tyr
236          20          25          30
237   atg gat cga tat gca aaa ctt gga gca att gct ttt act aac gca ctt      144
238   Met Asp Arg Tyr Ala Lys Leu Gly Ala Ile Ala Phe Thr Asn Ala Leu
239          35          40          45
240   acc ggt gtc gat tat acg tac gcc gaa tac tta gaa aaa tca tgc tgt      192
241   Thr Gly Val Asp Tyr Thr Tyr Ala Glu Tyr Leu Glu Lys Ser Cys Cys
242          50          55          60
243   cta gga gag gct tta aag aat tat ggt ttg gtt gtt gat gga aga att      240
244   Leu Gly Glu Ala Leu Lys Asn Tyr Gly Leu Val Val Asp Gly Arg Ile

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RAW SEQUENCE LISTING ERROR SUMMARY

DATE: 08/02/2004

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Input Set : N:\Crf3\RULE60\10829250.raw

Output Set: N:\CRF4\08022004\J829250.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 3

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/829,250

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TIME: 14:37:43

Input Set : N:\Crf3\RULE60\10829250.raw

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